

AMENDMENTS TO THE CLAIMS

Prior to examination of the application please amend the claims as follows:

1. (Original) A method for improving the specificity of a ligation reaction carried out between a first double stranded polynucleotide having a single stranded portion and a second polynucleotide having a complementary single stranded portion, said second polynucleotide being present in a sample comprising a mixture of different polynucleotides, comprising:

contacting the sample, under hybridising conditions, with the first polynucleotide and one or more third polynucleotide(s), wherein the third polynucleotide(s) comprises a single stranded portion that differs from the single stranded portion of the first polynucleotide by at least one base substitution, and carrying out a ligation reaction.

2. (Original) A method according to claim 1, wherein the third polynucleotide is a double stranded polynucleotide having said single stranded portion.

3. (Currently amended) A method according to claim 1 ~~or claim 2~~, wherein the single stranded portion on each of the first, second and third polynucleotides is from 3 to 6 bases in length.

4. (Currently amended) A method according to claim 3, wherein the single stranded portion is 4 bases in length.

5. (Currently amended) A method according to ~~any preceding claim~~, claim 1 wherein the single stranded portion of the third polynucleotide differs from the single stranded portion of the first polynucleotide by one base.

6. (Currently amended) A method according to ~~any preceding claim~~ claim 1, wherein the ligase is T4 DNA ligase.

7. (New) A method according to claim 2, wherein the single stranded portion on each of the first, second and third polynucleotides is from 3 to 6 bases in length.

8. (New) A method according to claim 7, wherein the single stranded portion is 4 bases in length.

9. (New) A method according to claim 2 wherein the single stranded portion of the third polynucleotide differs from the single stranded portion of the first polynucleotide by one base.

10. (New) A method according to claim 3 wherein the single stranded portion of the third polynucleotide differs from the single stranded portion of the first polynucleotide by one base.

11. (New) A method according to claim 4 wherein the single stranded portion of the third polynucleotide differs from the single stranded portion of the first polynucleotide by one base.

12. (New) A method according to claim 7 wherein the single stranded portion of the third polynucleotide differs from the single stranded portion of the first polynucleotide by one base.

13. (New) A method according to claim 8 wherein the single stranded portion of the third polynucleotide differs from the single stranded portion of the first polynucleotide by one base.

14. (New) A method according to claim 2, wherein the ligase is T4 DNA ligase.

15. (New) A method according to claim 3, wherein the ligase is T4 DNA ligase.

15. (New) A method according to claim 4, wherein the ligase is T4 DNA ligase.

16. (New) A method according to claim 5, wherein the ligase is T4 DNA ligase.

17. (New) A method according to claim 9, wherein the ligase is T4 DNA
ligase.
18. (New) A method according to claim 10, wherein the ligase is T4 DNA
ligase.
19. (New) A method according to claim 11, wherein the ligase is T4 DNA
ligase.
20. (New) A method according to claim 12, wherein the ligase is T4 DNA
ligase.
21. (New) A method according to claim 13, wherein the ligase is T4 DNA
ligase.